

# ***U.S. PATENT APPLICATION***

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***Invention:*** ISOLATED HUMAN DRUG-METABOLIZING PROTEINS, NUCLEIC  
ACID MOLECULES ENCODING HUMAN DRUG-METABOLIZING  
PROTEINS, AND USES THEREOF

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## ***SPECIFICATION***

# **ISOLATED HUMAN DRUG-METABOLIZING PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG-METABOLIZING PROTEINS, AND USES THEREOF**

## **RELATED APPLICATIONS**

The present application claims priority to provisional applications U.S. Serial No. 60/228,893 filed August 30, 2000 (Atty. Docket CL000763-PROV).

## **FIELD OF THE INVENTION**

The present invention is in the field of drug-metabolizing proteins that are related to the UDP-glucuronosyltransferase drug-metabolizing enzyme subfamily, recombinant DNA molecules and protein production. The present invention specifically provides novel drug-metabolizing peptides and proteins and nucleic acid molecules encoding such protein molecules, for use in the development of human therapeutics and human therapeutic development.

## **BACKGROUND OF THE INVENTION**

### Drug-Metabolizing Proteins

Induction of drug-metabolizing enzymes (“DMEs”) is a common biological response to xenobiotics, the mechanisms and consequences of which are important in academic, industrial, and regulatory areas of pharmacology and toxicology.

For most drugs, drug-metabolizing enzymes determine how long and how much of a drug remains in the body. Thus, developers of drugs recognize the importance of characterizing a drug candidate’s interaction with these enzymes. For example, polymorphisms of the drug-metabolizing enzyme CYP2D6, a member of the cytochrome p450 (“CYP”) superfamily, yield phenotypes of slow or ultra-rapid metabolizers of a wide spectrum of drugs including antidepressants, antipsychotics, beta-blockers, and antiarrhythmics. Such abnormal rates of drug metabolism can lead to drug ineffectiveness or to systemic accumulation and toxicity.

For pharmaceutical scientists developing a candidate drug, it is important know as early as possible in the design phase which enzymes metabolize the drug candidate and the speed with which they do it. Historically, the enzymes on a drug's metabolic pathway were determined through metabolism studies in animals, but this approach has now been largely supplanted by the use of human tissues or cloned drug-metabolizing enzymes to provide insights into the specific role of individual forms of these enzymes. Using these tools, the qualitative and quantitative fate of a drug candidate can be predicted prior to its first administration to humans. As a consequence, the selection and optimization of desirable characteristics of metabolism are possible early in the development process, thus avoiding unanticipated toxicity problems and associated costs subsequent to the drug's clinical investigation. Moreover, the effect of one drug on another's disposition can be inferred.

Known drug-metabolizing enzymes include the cytochrome p450 ("CYP") superfamily, N-acetyl transferases ("NAT"), UDP-glucuronosyl transferases ("UGT"), methyl transferases, alcohol dehydrogenase ("ADH"), aldehyde dehydrogenase ("ALDH"), dihydropyrimidine dehydrogenase ("DPD"), NADPH:quinone oxidoreductase ("NQO" or "DT diaphorase"), catechol O-methyltransferase ("COMT"), glutathione S-transferase ("GST"), histamine methyltransferase ("HMT"), sulfotransferases ("ST"), thiopurine methyltransferase ("TPMT"), and epoxide hydroxylase. Drug-metabolizing enzymes are generally classified into two phases according to their metabolic function. Phase I enzymes catalyze modification of functional groups, and phase II enzymes catalyze conjugation with endogenous substituents. These classifications should not be construed as exclusive nor exhaustive, as other mechanisms of drug metabolism have been discovered. For example, the use of active transport mechanisms been characterized as part of the process of detoxification.

Phase I reactions include catabolic processes such as deamination of aminases, hydrolysis of esters and amides, conjugation reactions with, for example, glycine or sulfate, oxidation by the cytochrome p450 oxidation/reduction enzyme system and degradation in the fatty acid pathway. Hydrolysis reactions occur mainly in the liver and plasma by a variety of non-specific hydrolases and esterases. Both deaminases and

amidases, also localized in the liver and serum, carry out a large part of the catabolic process. Reduction reactions occur mainly intracellularly in the endoplasmic reticulum.

Phase II enzymes detoxify toxic substances by catalyzing their conjugation with water-soluble substances, thus increasing toxins' solubility in water and increasing their rate of excretion. Additionally, conjugation reduces the toxins' biological reactivity. Examples of phase II enzymes include glutathione S-transferases and UDP-glucuronosyl transferases, which catalyze conjugation to glutathione and glucuronic acid, respectively. Transferases perform conjugation reactions mainly in the kidneys and liver.

The liver is the primary site of elimination of most drugs, including psychoactive drugs, and contains a plurality of both phase I and phase II enzymes that oxidize or conjugate drugs, respectively.

Physicians currently prescribe drugs and their dosages based on a population average and fail to take genetic variability into account. The variability between individuals in drug metabolism is usually due to both genetic and environmental factors, in particular, how the drug-metabolizing enzymes are controlled. With certain enzymes, the genetic component predominates and variability is associated with variants of the normal, wild-type enzyme.

Most drug-metabolizing enzymes exhibit clinically relevant genetic polymorphisms. Essentially all of the major human enzymes responsible for modification of functional groups or conjugation with endogenous substituents exhibit common polymorphisms at the genomic level. For example, polymorphisms expressing a non-functioning variant enzyme results in a sub-group of patients in the population who are more prone to the concentration-dependent effects of a drug. This sub-group of patients may show toxic side effects to a dose of drug that is otherwise without side effects in the general population. Recent development in genotyping allows identification of affected individuals. As a result, their atypical metabolism and likely response to a drug metabolized by the affected enzyme can be understood and predicted, thus permitting the physician to adjust the dose of drug they receive to achieve improved therapy.

A similar approach is also becoming important in identifying risk factors associated with the development of various cancers. This is because the enzymes

involved in drug metabolism are also responsible for the activation and detoxification of chemical carcinogens. Specifically, the development of neoplasia is regulated by a balance between phase I enzymes, which activate carcinogens, and phase II enzymes, which detoxify them. Accordingly, an individual's susceptibility to cancer often involves the balance between these two processes, which is, in part, genetically determined and can be screened by suitable genotyping tests. Higher induction of phase I enzymes compared to phase II enzymes results in the generation of large amounts of electrophiles and reactive oxygen species and may cause DNA and membrane damage and other adverse effects leading to neoplasia. Conversely, higher levels of phase II enzyme expression can protect cells from various chemical compounds.

Abnormal activity of drug-metabolizing enzymes has been implicated in a range of human diseases, including cancer, Parkinson's disease, myotonic dystrophy, and developmental defects.

### Cytochrome p450

An example of a phase I drug-metabolizing enzyme is the cytochrome p450 ("CYP") superfamily, the members of which comprise the major drug-metabolizing enzymes expressed in the liver. The CYP superfamily comprises heme proteins which catalyze the oxidation and dehydrogenation of a number of endogenous and exogenous lipophilic compounds. The CYP superfamily has immense diversity in its functions, with hundreds of isoforms in many species catalyzing many types of chemical reactions. The CYP superfamily comprises at least 30 related enzymes, which are divided into different families according to their amino acid homology. Examples of CYP families include CYP families 1, 2, 3 and 4, which comprise endoplasmic reticulum proteins responsible for the metabolism of drugs and other xenobiotics. Approximately 10-15 individual gene products within these four families metabolize thousands of structurally diverse compounds. It is estimated that collectively the enzymes in the CYP superfamily participate in the metabolism of greater than 80% of all available drugs used in humans. For example, the CYP 1A subfamily comprises CYP 1A2, which metabolizes several widely used drugs, including acetaminophen, amitriptyline, caffeine, clozapine, haloperidol, imipramine, olanzapine, ondansetron, phenacetin, propafenone, propranolol,

tacrine, theophylline, verapamil. In addition, CYP enzymes play additional roles in the metabolism of some endogenous substrates including prostaglandins and steroids.

Some CYP enzymes exist in a polymorphic form, meaning that a small percentage of the population possesses mutant genes that alter the activity of the enzyme, usually by diminishing or abolishing activity. For example, a genetic polymorphism has been well characterized with the CYP 2C19 and CYP 2D6 genes. Substrates of CYP 2C19 include clomipramine, diazepam, imipramine, mephenytoin, moclobemide, omeprazole, phenytoin, propranolol, and tolbutamide. Substrates of CYP 2D6 include alprenolol, amitriptyline, chlorpheniramine, clomipramine, codeine, desipramine, dextromethorphan, encainide, fluoxetine, haloperidol, imipramine, indoramin, metoprolol, nortriptyline, ondansetron, oxycodone, paroxetine, propranolol, and propafenone. Polymorphic variants of these genes metabolize these substrates at different rates, which can effect a patient's effective therapeutic dosage.

While the substrate specificity of CYPs must be very broad to accommodate the metabolism of all of these compounds, each individual CYP gene product has a narrower substrate specificity defined by its binding and catalytic sites. Drug metabolism can thereby be regulated by changes in the amount or activity of specific CYP gene products. Methods of CYP regulation include genetic differences in the expression of CYP gene products (i.e., genetic polymorphisms), inhibition of CYP metabolism by other xenobiotics that also bind to the CYP, and induction of certain CYPs by the drug itself or other xenobiotics. Inhibition and induction of CYPs is one of the most common mechanisms of adverse drug interactions. For example, the CYP3A subfamily is involved in clinically significant drug interactions involving nonsedating antihistamines and cisapride that may result in cardiac dysrhythmias. In another example, CYP3A4 and CYP1A2 enzymes are involved in drug interactions involving theophylline. In yet another example, CYP2D6 is responsible for the metabolism of many psychotherapeutic agents. Additionally, CYP enzymes metabolize the protease inhibitors used to treat patients infected with the human immunodeficiency virus. By understanding the unique functions and characteristics of these enzymes, physicians may better anticipate and manage drug interactions and may predict or explain an individual's response to a particular therapeutic regimen.

Examples of reactions catalyzed by the CYP superfamily include peroxidative reactions utilizing peroxides as oxygen donors in hydroxylation reactions, as substrates for reductive beta-scission, and as peroxyhemiacetal intermediates in the cleavage of aldehydes to formate and alkenes. Lipid hydroperoxides undergo reductive beta-cleavage to give hydrocarbons and aldehydic acids. One of these products, trans-4-hydroxynonenal, inactivates CYP, particularly alcohol-inducible 2E1, in what may be a negative regulatory process. Although a CYP iron-oxene species is believed to be the oxygen donor in most hydroxylation reactions, an iron-peroxy species is apparently involved in the deformylation of many aldehydes with desaturation of the remaining structure, as in aromatization reactions.

Examples of drugs with oxidative metabolism associated with CYP enzymes include acetaminophen, alfentanil, alprazolam, alprenolol, amiodarone, amitriptyline, astemizole, buspirone, caffeine, carbamazepine, chlorpheniramine, cisapride, clomipramine, clomipramine, clozapine, codeine, colchicine, cortisol, cyclophosphamide, cyclosporine, dapsone, desipramine, dextromethorphan, diazepam, diclofenac, diltiazem, encainide, erythromycin, estradiol, felodipine, fluoxetine, fluvastatin, haloperidol, ibuprofen, imipramine, indinavir, indomethacin, indoramin, irbesartan, lidocaine, losartan, macrolide antibiotics, mephenytoin, methadone, metoprolol, mexilitene, midazolam, moclobemide, naproxen, nefazodone, nifedipine, nifedipine, nitrendipine, nortriptyline, olanzapine, omeprazole, ondansetron, oxycodone, paclitaxel, paroxetine, phenacetin, phenytoin, piroxicam, progesterone, propafenone, propranolol, quinidine, ritonavir, saquinavir, sertraline, sildenafil, S-warfarin, tacrine, tamoxifen, tenoxicam, terfenadine, testosterone, theophylline, timolol, tolbutamide, triazolam, verapamil, and vinblastine.

Abnormal activity of phase I enzymes has been implicated in a range of human diseases. For example, enhanced CYP2D6 activity has been related to malignancies of the bladder, liver, pharynx, stomach and lungs, whereas decreased CYP2D activity has been linked to an increased risk of Parkinson's disease. Other syndromes and developmental defects associated with deficiencies in the CYP superfamily include cerebrotendinous xanthomatosis, adrenal hyperplasia, gynecomastia, and myotonic dystrophy.

The CYP superfamily a major target for drug action and development. Accordingly, it is valuable to the field of pharmaceutical development to identify and characterize previously unknown members of the CYP superfamily.

#### UDP-glucuronosyltransferases

Potential drug interactions involving phase II metabolism are increasingly being recognized. An important group of phase II enzymes involved in drug metabolism are the glucuronosyltransferases, especially the UDP-glucuronyltransferase ("UGT") superfamily. Members of the UGT superfamily catalyze the enzymatic addition of UDP glucuronic acid as a sugar donor to fat-soluble chemicals, a process which increases their solubility in water and increases their rate of excretion. In mammals, glucuronic acid is the main sugar that is used to prevent the accumulation of waste products of metabolism and fat-soluble chemicals from the environment to toxic levels in the body. Both inducers and inhibitors of glucuronosyltransferases are known and have the potential to affect the plasma concentration and actions of important drugs, including psychotropic drugs.

The UGT superfamily comprises several families of enzymes in several species defined with a nomenclature similar to that used to define members of the CYP superfamily. In animals, yeast, plants and bacteria there are at least 110 distinct known members of the UGT superfamily. As many as 33 families have been defined, with three families identified in humans. Different UGT families are defined as having <45% amino acid sequence homology; within subfamilies there is approximately 60% homology. The members of the UGT superfamily are part of a further superfamily of UDP glycosyltransferases found in animals, plants and bacteria.

The role of phase II enzymes, and of UGT enzymes in particular, is being increasingly recognized as important in psychopharmacology. UGT enzymes conjugate many important psychotropic drugs and are an important source of variability in drug response and drug interactions. For example, the benzodiazepines lorazepam, oxazepam, and temazepam undergo phase II reactions exclusively before being excreted into the urine.



Phase II enzymes metabolize and detoxify hazardous substances, such as carcinogens. The expression of genes encoding phase II enzymes is known to be up-regulated by hundreds of agents. For example, oltipraz is known to up-regulate phase II enzyme expression. Studies have demonstrated protection from the cancer-causing effects of carcinogens when selected phase II enzyme inducers are administered prior to the carcinogens. The potential use of phase II enzyme inducers in humans for prevention of cancers related to exposure to carcinogens has prompted studies aimed at understanding their molecular effects. Current biochemical and molecular biological research methodologies can be used to identify and characterize selective phase II enzyme inducers and their targets. Identification of genes responding to cancer chemopreventive agents will facilitate studies of their basic mechanism and provide insights about the relationship between gene regulation, enzyme polymorphism, and carcinogen detoxification.

Examples of drugs with conjugative metabolism associated with UGT enzymes include amitriptyline, buprenorphine, chlorpromazine, clozapine, codeine, cyproheptadine, dihydrocodeine, doxepin, imipramine, lamotrigine, lorazepam, morphine, naltrexone, naltrexone, temazepam, and valproate.

Abnormal activity of phase II enzymes has been implicated in a range of human diseases. For example, Gilbert syndrome is an autosomal dominant disorder caused by mutation in the UGT1 gene, and mutations in the UGT1A1 enzyme have been demonstrated to be responsible for Crigler-Najjar syndrome.

The UGT superfamily a major target for drug action and development. Accordingly, it is valuable to the field of pharmaceutical development to identify and characterize previously unknown members of the UGT superfamily.

For a further review of UDP-glucuronosyltransferases, see Jin et al., *Biochem Biophys Res Commun* 1993 Jul 15;194(1):496-503; Beaulieu et al., *Biochem Biophys Res Commun* 1998 Jul 9;248(1):44-50; Belanger et al., *DNA Cell Biol* 1997 Oct;16(10):1195-205; Jackson et al., *Biochem J* 1987 Mar 1;242(2):581-8; Taura et al., *Biochem Biophys Res Commun* 2000 Jul 14;273(3):1048-1052; Burchell et al., *DNA Cell Biol*. 10: 487-494, 1991; Krasnewich et al., *Somat. Cell Molec. Genet.* 13: 179-182, 1987; Monaghan et al.,

*Genomics* 23: 496-499, 1994; Monaghan *et al.*, *Genomics* 13: 908-909, 1992; and Riedy *et al.*, *Pharmacogenetics* 10: 251-260, 2000.

Drug-metabolizing enzymes, particularly members of the UDP-glucuronosyltransferase drug-metabolizing enzyme subfamily, are a major target for drug action and development. Accordingly, it is valuable to the field of pharmaceutical development to identify and characterize previously unknown members of this subfamily of drug-metabolizing proteins. The present invention advances the state of the art by providing a previously unidentified human drug-metabolizing proteins that have homology to members of the UDP-glucuronosyltransferase drug-metabolizing enzyme subfamily.

## SUMMARY OF THE INVENTION

The present invention is based in part on the identification of amino acid sequences of human drug-metabolizing enzyme peptides and proteins that are related to the UDP-glucuronosyltransferase drug-metabolizing enzyme subfamily, as well as allelic variants and other mammalian orthologs thereof. These unique peptide sequences, and nucleic acid sequences that encode these peptides, can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic agents that modulate drug-metabolizing enzyme activity in cells and tissues that express the drug-metabolizing enzyme. Experimental data as provided in Figure 1 indicates expression in humans in the kidney (including kidney hypernephromas), liver (including fetal liver, HepG2 cell lines, and hepatocellular carcinomas), and pigmental retinal epithelium.

## DESCRIPTION OF THE FIGURE SHEETS

FIGURE 1 provides the nucleotide sequence of a cDNA molecule that encodes the drug-metabolizing enzyme protein of the present invention. (SEQ ID NO:1) In addition, structure and functional information is provided, such as ATG start, stop and tissue distribution, where available, that allows one to readily determine specific uses of inventions based on this molecular sequence. Experimental data as provided in Figure 1 indicates expression in humans in the kidney (including kidney hypernephromas), liver

(including fetal liver, HepG2 cell lines, and hepatocellular carcinomas), and pigmental retinal epithelium.

FIGURE 2 provides the predicted amino acid sequence of the drug-metabolizing enzyme of the present invention. (SEQ ID NO:2) In addition structure and functional information such as protein family, function, and modification sites is provided where available, allowing one to readily determine specific uses of inventions based on this molecular sequence.

FIGURE 3 provides genomic sequences that span the gene encoding the drug-metabolizing enzyme protein of the present invention. (SEQ ID NO:3) In addition structure and functional information, such as intron/exon structure, promoter location, etc., is provided where available, allowing one to readily determine specific uses of inventions based on this molecular sequence. As illustrated in Figure 3, SNPs were identified at 17 different nucleotide positions.

## **DETAILED DESCRIPTION OF THE INVENTION**

### General Description

The present invention is based on the sequencing of the human genome. During the sequencing and assembly of the human genome, analysis of the sequence information revealed previously unidentified fragments of the human genome that encode peptides that share structural and/or sequence homology to protein/peptide/domains identified and characterized within the art as being a drug-metabolizing enzyme protein or part of a drug-metabolizing enzyme protein and are related to the UDP-glucuronosyltransferase drug-metabolizing enzyme subfamily. Utilizing these sequences, additional genomic sequences were assembled and transcript and/or cDNA sequences were isolated and characterized. Based on this analysis, the present invention provides amino acid sequences of human drug-metabolizing enzyme peptides and proteins that are related to the UDP-glucuronosyltransferase drug-metabolizing enzyme subfamily, nucleic acid sequences in the form of transcript sequences, cDNA sequences and/or genomic sequences that encode these drug-metabolizing enzyme peptides and proteins, nucleic acid variation (allelic information), tissue distribution of expression, and information

about the closest art known protein/peptide/domain that has structural or sequence homology to the drug-metabolizing enzyme of the present invention.

In addition to being previously unknown, the peptides that are provided in the present invention are selected based on their ability to be used for the development of commercially important products and services. Specifically, the present peptides are selected based on homology and/or structural relatedness to known drug-metabolizing enzyme proteins of the UDP-glucuronosyltransferase drug-metabolizing enzyme subfamily and the expression pattern observed. Experimental data as provided in Figure 1 indicates expression in humans in the kidney (including kidney hypernephromas), liver (including fetal liver, HepG2 cell lines, and hepatocellular carcinomas), and pigmental retinal epithelium. The art has clearly established the commercial importance of members of this family of proteins and proteins that have expression patterns similar to that of the present gene. Some of the more specific features of the peptides of the present invention, and the uses thereof, are described herein, particularly in the Background of the Invention and in the annotation provided in the Figures, and/or are known within the art for each of the known UDP-glucuronosyltransferase family or subfamily of drug-metabolizing enzyme proteins.

### Specific Embodiments

#### Peptide Molecules

The present invention provides nucleic acid sequences that encode protein molecules that have been identified as being members of the drug-metabolizing enzyme family of proteins and are related to the UDP-glucuronosyltransferase drug-metabolizing enzyme subfamily (protein sequences are provided in Figure 2, transcript/cDNA sequences are provided in Figure 1 and genomic sequences are provided in Figure 3). The peptide sequences provided in Figure 2, as well as the obvious variants described herein, particularly allelic variants as identified herein and using the information in Figure 3, will be referred herein as the drug-metabolizing enzyme peptides of the present invention, drug-metabolizing enzyme peptides, or peptides/proteins of the present invention.

The present invention provides isolated peptide and protein molecules that consist of, consist essentially of, or comprise the amino acid sequences of the drug-metabolizing enzyme peptides disclosed in the Figure 2, (encoded by the nucleic acid molecule shown in Figure 1, transcript/cDNA or Figure 3, genomic sequence), as well as all obvious variants of these peptides that are within the art to make and use. Some of these variants are described in detail below.

As used herein, a peptide is said to be "isolated" or "purified" when it is substantially free of cellular material or free of chemical precursors or other chemicals. The peptides of the present invention can be purified to homogeneity or other degrees of purity. The level of purification will be based on the intended use. The critical feature is that the preparation allows for the desired function of the peptide, even if in the presence of considerable amounts of other components (the features of an isolated nucleic acid molecule is discussed below).

In some uses, "substantially free of cellular material" includes preparations of the peptide having less than about 30% (by dry weight) other proteins (i.e., contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less than about 5% other proteins. When the peptide is recombinantly produced, it can also be substantially free of culture medium, i.e., culture medium represents less than about 20% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of the peptide in which it is separated from chemical precursors or other chemicals that are involved in its synthesis. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of the drug-metabolizing enzyme peptide having less than about 30% (by dry weight) chemical precursors or other chemicals, less than about 20% chemical precursors or other chemicals, less than about 10% chemical precursors or other chemicals, or less than about 5% chemical precursors or other chemicals.

The isolated drug-metabolizing enzyme peptide can be purified from cells that naturally express it, purified from cells that have been altered to express it (recombinant), or synthesized using known protein synthesis methods. Experimental data as provided in Figure 1 indicates expression in humans in the kidney (including kidney hypernephromas),

liver (including fetal liver, HepG2 cell lines, and hepatocellular carcinomas), and pigmental retinal epithelium. For example, a nucleic acid molecule encoding the drug-metabolizing enzyme peptide is cloned into an expression vector, the expression vector introduced into a host cell and the protein expressed in the host cell. The protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Many of these techniques are described in detail below.

Accordingly, the present invention provides proteins that consist of the amino acid sequences provided in Figure 2 (SEQ ID NO:2), for example, proteins encoded by the transcript/cDNA nucleic acid sequences shown in Figure 1 (SEQ ID NO:1) and the genomic sequences provided in Figure 3 (SEQ ID NO:3). The amino acid sequence of such a protein is provided in Figure 2. A protein consists of an amino acid sequence when the amino acid sequence is the final amino acid sequence of the protein.

The present invention further provides proteins that consist essentially of the amino acid sequences provided in Figure 2 (SEQ ID NO:2), for example, proteins encoded by the transcript/cDNA nucleic acid sequences shown in Figure 1 (SEQ ID NO:1) and the genomic sequences provided in Figure 3 (SEQ ID NO:3). A protein consists essentially of an amino acid sequence when such an amino acid sequence is present with only a few additional amino acid residues, for example from about 1 to about 100 or so additional residues, typically from 1 to about 20 additional residues in the final protein.

The present invention further provides proteins that comprise the amino acid sequences provided in Figure 2 (SEQ ID NO:2), for example, proteins encoded by the transcript/cDNA nucleic acid sequences shown in Figure 1 (SEQ ID NO:1) and the genomic sequences provided in Figure 3 (SEQ ID NO:3). A protein comprises an amino acid sequence when the amino acid sequence is at least part of the final amino acid sequence of the protein. In such a fashion, the protein can be only the peptide or have additional amino acid molecules, such as amino acid residues (contiguous encoded sequence) that are naturally associated with it or heterologous amino acid residues/peptide sequences. Such a protein can have a few additional amino acid residues or can comprise several hundred or more additional amino acids. The preferred classes of proteins that are comprised of the drug-metabolizing enzyme peptides of the present invention are the naturally occurring

mature proteins. A brief description of how various types of these proteins can be made/isolated is provided below.

The drug-metabolizing enzyme peptides of the present invention can be attached to heterologous sequences to form chimeric or fusion proteins. Such chimeric and fusion proteins comprise a drug-metabolizing enzyme peptide operatively linked to a heterologous protein having an amino acid sequence not substantially homologous to the drug-metabolizing enzyme peptide. "Operatively linked" indicates that the drug-metabolizing enzyme peptide and the heterologous protein are fused in-frame. The heterologous protein can be fused to the N-terminus or C-terminus of the drug-metabolizing enzyme peptide.

In some uses, the fusion protein does not affect the activity of the drug-metabolizing enzyme peptide *per se*. For example, the fusion protein can include, but is not limited to, enzymatic fusion proteins, for example beta-galactosidase fusions, yeast two-hybrid GAL fusions, poly-His fusions, MYC-tagged, HI-tagged and Ig fusions. Such fusion proteins, particularly poly-His fusions, can facilitate the purification of recombinant drug-metabolizing enzyme peptide. In certain host cells (e.g., mammalian host cells), expression and/or secretion of a protein can be increased by using a heterologous signal sequence.

A chimeric or fusion protein can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different protein sequences are ligated together in-frame in accordance with conventional techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and re-amplified to generate a chimeric gene sequence (see Ausubel *et al.*, *Current Protocols in Molecular Biology*, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST protein). A drug-metabolizing enzyme peptide-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the drug-metabolizing enzyme peptide.

As mentioned above, the present invention also provides and enables obvious variants of the amino acid sequence of the proteins of the present invention, such as naturally occurring mature forms of the peptide, allelic/sequence variants of the peptides,

non-naturally occurring recombinantly derived variants of the peptides, and orthologs and paralogs of the peptides. Such variants can readily be generated using art-known techniques in the fields of recombinant nucleic acid technology and protein biochemistry. It is understood, however, that variants exclude any amino acid sequences disclosed prior to the invention.

Such variants can readily be identified/made using molecular techniques and the sequence information disclosed herein. Further, such variants can readily be distinguished from other peptides based on sequence and/or structural homology to the drug-metabolizing enzyme peptides of the present invention. The degree of homology/identity present will be based primarily on whether the peptide is a functional variant or non-functional variant, the amount of divergence present in the paralog family and the evolutionary distance between the orthologs.

To determine the percent identity of two amino acid sequences or two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). In a preferred embodiment, at least 30%, 40%, 50%, 60%, 70%, 80%, or 90% or more of the length of a reference sequence is aligned for comparison purposes. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position (as used herein amino acid or nucleic acid "identity" is equivalent to amino acid or nucleic acid "homology"). The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences.

The comparison of sequences and determination of percent identity and similarity between two sequences can be accomplished using a mathematical algorithm.

(*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press,



New York, 1993; *Computer Analysis of Sequence Data, Part 1*, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blossom 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (Devereux, J., *et al.*, *Nucleic Acids Res.* 12(1):387 (1984)) (available at <http://www.gcg.com>), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Myers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against sequence databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (*J. Mol. Biol.* 215:403-10 (1990)). BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to the nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to the proteins of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (*Nucleic Acids Res.* 25(17):3389-3402 (1997)). When utilizing BLAST and gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used.

Full-length pre-processed forms, as well as mature processed forms, of proteins that comprise one of the peptides of the present invention can readily be identified as having complete sequence identity to one of the drug-metabolizing enzyme peptides of the present invention as well as being encoded by the same genetic locus as the drug-metabolizing enzyme peptide provided herein. The gene encoding the novel drug-metabolizing protein of the present invention is located on a genome component that has been mapped to human chromosome 4 (as indicated in Figure 3), which is supported by multiple lines of evidence, such as STS and BAC map data.

Allelic variants of a drug-metabolizing enzyme peptide can readily be identified as being a human protein having a high degree (significant) of sequence homology/identity to at least a portion of the drug-metabolizing enzyme peptide as well as being encoded by the same genetic locus as the drug-metabolizing enzyme peptide provided herein. Genetic locus can readily be determined based on the genomic information provided in Figure 3, such as the genomic sequence mapped to the reference human. The gene encoding the novel drug-metabolizing protein of the present invention is located on a genome component that has been mapped to human chromosome 4 (as indicated in Figure 3), which is supported by multiple lines of evidence, such as STS and BAC map data. As used herein, two proteins (or a region of the proteins) have significant homology when the amino acid sequences are typically at least about 70-80%, 80-90%, and more typically at least about 90-95% or more homologous. A significantly homologous amino acid sequence, according to the present invention, will be encoded by a nucleic acid sequence that will hybridize to a drug-metabolizing enzyme peptide encoding nucleic acid molecule under stringent conditions as more fully described below.

Figure 3 provides information on SNPs that have been found in the gene encoding the drug-metabolizing protein of the present invention. SNPs were identified at 17 different nucleotide positions. Some of these SNPs may affect control/regulatory elements.

Paralogs of a drug-metabolizing enzyme peptide can readily be identified as having some degree of significant sequence homology/identity to at least a portion of the drug-metabolizing enzyme peptide, as being encoded by a gene from humans, and as having similar activity or function. Two proteins will typically be considered paralogs when the

amino acid sequences are typically at least about 60% or greater, and more typically at least about 70% or greater homology through a given region or domain. Such paralogs will be encoded by a nucleic acid sequence that will hybridize to a drug-metabolizing enzyme peptide encoding nucleic acid molecule under moderate to stringent conditions as more fully described below.

Orthologs of a drug-metabolizing enzyme peptide can readily be identified as having some degree of significant sequence homology/identity to at least a portion of the drug-metabolizing enzyme peptide as well as being encoded by a gene from another organism. Preferred orthologs will be isolated from mammals, preferably primates, for the development of human therapeutic targets and agents. Such orthologs will be encoded by a nucleic acid sequence that will hybridize to a drug-metabolizing enzyme peptide encoding nucleic acid molecule under moderate to stringent conditions, as more fully described below, depending on the degree of relatedness of the two organisms yielding the proteins.

Non-naturally occurring variants of the drug-metabolizing enzyme peptides of the present invention can readily be generated using recombinant techniques. Such variants include, but are not limited to deletions, additions and substitutions in the amino acid sequence of the drug-metabolizing enzyme peptide. For example, one class of substitutions are conserved amino acid substitution. Such substitutions are those that substitute a given amino acid in a drug-metabolizing enzyme peptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu, and Ile; interchange of the hydroxyl residues Ser and Thr; exchange of the acidic residues Asp and Glu; substitution between the amide residues Asn and Gln; exchange of the basic residues Lys and Arg; and replacements among the aromatic residues Phe and Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie *et al.*, *Science* 247:1306-1310 (1990).

Variant drug-metabolizing enzyme peptides can be fully functional or can lack function in one or more activities, e.g. ability to bind substrate, ability to phosphorylate substrate, ability to mediate signaling, etc. Fully functional variants typically contain only conservative variation or variation in non-critical residues or in non-critical regions. Figure

2 provides the result of protein analysis and can be used to identify critical domains/regions. Functional variants can also contain substitution of similar amino acids that result in no change or an insignificant change in function. Alternatively, such substitutions may positively or negatively affect function to some degree.

Non-functional variants typically contain one or more non-conservative amino acid substitutions, deletions, insertions, inversions, or truncation or a substitution, insertion, inversion, or deletion in a critical residue or critical region.

Amino acids that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham *et al.*, *Science* 244:1081-1085 (1989)), particularly using the results provided in Figure 2. The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity such as drug-metabolizing enzyme activity or in assays such as an *in vitro* proliferative activity. Sites that are critical for binding partner/substrate binding can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol.* 224:899-904 (1992); de Vos *et al.* *Science* 255:306-312 (1992)).

The present invention further provides fragments of the drug-metabolizing enzyme peptides, in addition to proteins and peptides that comprise and consist of such fragments, particularly those comprising the residues identified in Figure 2. The fragments to which the invention pertains, however, are not to be construed as encompassing fragments that may be disclosed publicly prior to the present invention.

As used herein, a fragment comprises at least 8, 10, 12, 14, 16, or more contiguous amino acid residues from a drug-metabolizing enzyme peptide. Such fragments can be chosen based on the ability to retain one or more of the biological activities of the drug-metabolizing enzyme peptide or could be chosen for the ability to perform a function, e.g. bind a substrate or act as an immunogen. Particularly important fragments are biologically active fragments, peptides that are, for example, about 8 or more amino acids in length. Such fragments will typically comprise a domain or motif of the drug-metabolizing enzyme peptide, e.g., active site, a transmembrane domain or a substrate-binding domain. Further, possible fragments include, but are not limited to, domain or motif containing fragments, soluble peptide fragments, and fragments containing immunogenic structures. Predicted

domains and functional sites are readily identifiable by computer programs well known and readily available to those of skill in the art (e.g., PROSITE analysis). The results of one such analysis are provided in Figure 2.

Polypeptides often contain amino acids other than the 20 amino acids commonly referred to as the 20 naturally occurring amino acids. Further, many amino acids, including the terminal amino acids, may be modified by natural processes, such as processing and other post-translational modifications, or by chemical modification techniques well known in the art. Common modifications that occur naturally in drug-metabolizing enzyme peptides are described in basic texts, detailed monographs, and the research literature, and they are well known to those of skill in the art (some of these features are identified in Figure 2).

Known modifications include, but are not limited to, acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent crosslinks, formation of cystine, formation of pyroglutamate, formylation, gamma carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination.

Such modifications are well known to those of skill in the art and have been described in great detail in the scientific literature. Several particularly common modifications, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation, for instance, are described in most basic texts, such as *Proteins - Structure and Molecular Properties*, 2nd Ed., T.E. Creighton, W. H. Freeman and Company, New York (1993). Many detailed reviews are available on this subject, such as by Wold, F., *Posttranslational Covalent Modification of Proteins*, B.C. Johnson, Ed., Academic Press, New York 1-12 (1983); Seifter *et al.* (*Meth. Enzymol.* 182: 626-646 (1990)) and Rattan *et al.* (*Ann. N.Y. Acad. Sci.* 663:48-62 (1992)).

Accordingly, the drug-metabolizing enzyme peptides of the present invention also encompass derivatives or analogs in which a substituted amino acid residue is not one encoded by the genetic code, in which a substituent group is included, in which the mature drug-metabolizing enzyme peptide is fused with another compound, such as a compound to increase the half-life of the drug-metabolizing enzyme peptide (for example, polyethylene glycol), or in which the additional amino acids are fused to the mature drug-metabolizing enzyme peptide, such as a leader or secretory sequence or a sequence for purification of the mature drug-metabolizing enzyme peptide or a pro-protein sequence.

### Protein/Peptide Uses

The proteins of the present invention can be used in substantial and specific assays related to the functional information provided in the Figures; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its binding partner or ligand) in biological fluids; and as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state). Where the protein binds or potentially binds to another protein or ligand (such as, for example, in a drug-metabolizing enzyme-effector protein interaction or drug-metabolizing enzyme-ligand interaction), the protein can be used to identify the binding partner/ligand so as to develop a system to identify inhibitors of the binding interaction. Any or all of these uses are capable of being developed into reagent grade or kit format for commercialization as commercial products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

The potential uses of the peptides of the present invention are based primarily on the source of the protein as well as the class/action of the protein. For example, drug-metabolizing enzymes isolated from humans and their human/mammalian orthologs

serve as targets for identifying agents for use in mammalian therapeutic applications, e.g. a human drug, particularly in modulating a biological or pathological response in a cell or tissue that expresses the drug-metabolizing enzyme. Experimental data as provided in Figure 1 indicates that the drug-metabolizing proteins of the present invention are expressed in humans in the kidney (including kidney hypernephromas), liver (including HepG2 cell lines and hepatocellular carcinomas), and pigmental retinal epithelium, as indicated by virtual northern blot analysis. In addition, PCR-based tissue screening panels indicate expression in human fetal liver. A large percentage of pharmaceutical agents are being developed that modulate the activity of drug-metabolizing enzyme proteins, particularly members of the UDP-glucuronosyltransferase subfamily (see Background of the Invention). The structural and functional information provided in the Background and Figures provide specific and substantial uses for the molecules of the present invention, particularly in combination with the expression information provided in Figure 1. Experimental data as provided in Figure 1 indicates expression in humans in the kidney (including kidney hypernephromas), liver (including fetal liver, HepG2 cell lines, and hepatocellular carcinomas), and pigmental retinal epithelium. Such uses can readily be determined using the information provided herein, that which is known in the art, and routine experimentation.

The drug-metabolizing enzyme polypeptides (including variants and fragments that may have been disclosed prior to the present invention) are useful for biological assays related to drug-metabolizing enzymes that are related to members of the UDP-glucuronosyltransferase subfamily. Such assays involve any of the known drug-metabolizing enzyme functions or activities or properties useful for diagnosis and treatment of drug-metabolizing enzyme-related conditions that are specific for the subfamily of drug-metabolizing enzymes that the one of the present invention belongs to, particularly in cells and tissues that express the drug-metabolizing enzyme. Experimental data as provided in Figure 1 indicates that the drug-metabolizing proteins of the present invention are expressed in humans in the kidney (including kidney hypernephromas), liver (including HepG2 cell lines and hepatocellular carcinomas), and pigmental retinal epithelium, as indicated by virtual northern blot analysis. In addition, PCR-based tissue screening panels indicate expression in human fetal liver.

The drug-metabolizing enzyme polypeptides are also useful in drug screening assays, in cell-based or cell-free systems. Cell-based systems can be native, i.e., cells that normally express the drug-metabolizing enzyme, as a biopsy or expanded in cell culture. Experimental data as provided in Figure 1 indicates expression in humans in the kidney (including kidney hypernephromas), liver (including fetal liver, HepG2 cell lines, and hepatocellular carcinomas), and pigmental retinal epithelium. In an alternate embodiment, cell-based assays involve recombinant host cells expressing the drug-metabolizing enzyme protein.

The polypeptides can be used to identify compounds that modulate drug-metabolizing enzyme activity of the protein in its natural state or an altered form that causes a specific disease or pathology associated with the drug-metabolizing enzyme. Both the drug-metabolizing enzymes of the present invention and appropriate variants and fragments can be used in high-throughput screens to assay candidate compounds for the ability to bind to the drug-metabolizing enzyme. These compounds can be further screened against a functional drug-metabolizing enzyme to determine the effect of the compound on the drug-metabolizing enzyme activity. Further, these compounds can be tested in animal or invertebrate systems to determine activity/effectiveness. Compounds can be identified that activate (agonist) or inactivate (antagonist) the drug-metabolizing enzyme to a desired degree.

Further, the drug-metabolizing enzyme polypeptides can be used to screen a compound for the ability to stimulate or inhibit interaction between the drug-metabolizing enzyme protein and a molecule that normally interacts with the drug-metabolizing enzyme protein. Such assays typically include the steps of combining the drug-metabolizing enzyme protein with a candidate compound under conditions that allow the drug-metabolizing enzyme protein, or fragment, to interact with the target molecule, and to detect the formation of a complex between the protein and the target or to detect the biochemical consequence of the interaction with the drug-metabolizing enzyme protein and the target.

Candidate compounds include, for example, 1) peptides such as soluble peptides, including Ig-tailed fusion peptides and members of random peptide libraries (see, e.g., Lam *et al.*, *Nature* 354:82-84 (1991); Houghten *et al.*, *Nature* 354:84-86 (1991)) and combinatorial chemistry-derived molecular libraries made of D- and/or L- configuration



amino acids; 2) phosphopeptides (e.g., members of random and partially degenerate, directed phosphopeptide libraries, see, e.g., Songyang *et al.*, *Cell* 72:767-778 (1993)); 3) antibodies (e.g., polyclonal, monoclonal, humanized, anti-idiotypic, chimeric, and single chain antibodies as well as Fab, F(ab')<sub>2</sub>, Fab expression library fragments, and epitope-binding fragments of antibodies); and 4) small organic and inorganic molecules (e.g., molecules obtained from combinatorial and natural product libraries).

One candidate compound is a soluble fragment of the receptor that competes for substrate binding. Other candidate compounds include mutant drug-metabolizing enzymes or appropriate fragments containing mutations that affect drug-metabolizing enzyme function and thus compete for substrate. Accordingly, a fragment that competes for substrate, for example with a higher affinity, or a fragment that binds substrate but does not allow release, is encompassed by the invention.

Any of the biological or biochemical functions mediated by the drug-metabolizing enzyme can be used as an endpoint assay. These include all of the biochemical or biochemical/biological events described herein, in the references cited herein, incorporated by reference for these endpoint assay targets, and other functions known to those of ordinary skill in the art or that can be readily identified using the information provided in the Figures, particularly Figure 2. Specifically, a biological function of a cell or tissues that expresses the drug-metabolizing enzyme can be assayed. Experimental data as provided in Figure 1 indicates that the drug-metabolizing proteins of the present invention are expressed in humans in the kidney (including kidney hypernephromas), liver (including HepG2 cell lines and hepatocellular carcinomas), and pigmental retinal epithelium, as indicated by virtual northern blot analysis. In addition, PCR-based tissue screening panels indicate expression in human fetal liver.

Binding and/or activating compounds can also be screened by using chimeric drug-metabolizing enzyme proteins in which the amino terminal extracellular domain, or parts thereof, the entire transmembrane domain or subregions, such as any of the seven transmembrane segments or any of the intracellular or extracellular loops and the carboxy terminal intracellular domain, or parts thereof, can be replaced by heterologous domains or subregions. For example, a substrate-binding region can be used that interacts with a different substrate than that which is recognized by the native drug-metabolizing enzyme.

Accordingly, a different set of signal transduction components is available as an end-point assay for activation. This allows for assays to be performed in other than the specific host cell from which the drug-metabolizing enzyme is derived.

The drug-metabolizing enzyme polypeptides are also useful in competition binding assays in methods designed to discover compounds that interact with the drug-metabolizing enzyme (e.g. binding partners and/or ligands). Thus, a compound is exposed to a drug-metabolizing enzyme polypeptide under conditions that allow the compound to bind or to otherwise interact with the polypeptide. Soluble drug-metabolizing enzyme polypeptide is also added to the mixture. If the test compound interacts with the soluble drug-metabolizing enzyme polypeptide, it decreases the amount of complex formed or activity from the drug-metabolizing enzyme target. This type of assay is particularly useful in cases in which compounds are sought that interact with specific regions of the drug-metabolizing enzyme. Thus, the soluble polypeptide that competes with the target drug-metabolizing enzyme region is designed to contain peptide sequences corresponding to the region of interest.

To perform cell free drug screening assays, it is sometimes desirable to immobilize either the drug-metabolizing enzyme protein, or fragment, or its target molecule to facilitate separation of complexes from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay.

Techniques for immobilizing proteins on matrices can be used in the drug screening assays. In one embodiment, a fusion protein can be provided which adds a domain that allows the protein to be bound to a matrix. For example, glutathione-S-transferase fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtitre plates, which are then combined with the cell lysates (e.g., <sup>35</sup>S-labeled) and the candidate compound, and the mixture incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads are washed to remove any unbound label, and the matrix immobilized and radiolabel determined directly, or in the supernatant after the complexes are dissociated. Alternatively, the complexes can be dissociated from the matrix, separated by SDS-PAGE, and the level of drug-metabolizing enzyme-binding protein found in the bead fraction quantitated from the gel using standard electrophoretic techniques. For example, either the polypeptide or its target molecule can be immobilized utilizing

conjugation of biotin and streptavidin using techniques well known in the art. Alternatively, antibodies reactive with the protein but which do not interfere with binding of the protein to its target molecule can be derivatized to the wells of the plate, and the protein trapped in the wells by antibody conjugation. Preparations of a drug-metabolizing enzyme-binding protein and a candidate compound are incubated in the drug-metabolizing enzyme protein-presenting wells and the amount of complex trapped in the well can be quantitated. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the drug-metabolizing enzyme protein target molecule, or which are reactive with drug-metabolizing enzyme protein and compete with the target molecule, as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the target molecule.

Agents that modulate one of the drug-metabolizing enzymes of the present invention can be identified using one or more of the above assays, alone or in combination. It is generally preferable to use a cell-based or cell free system first and then confirm activity in an animal or other model system. Such model systems are well known in the art and can readily be employed in this context.

Modulators of drug-metabolizing enzyme protein activity identified according to these drug screening assays can be used to treat a subject with a disorder mediated by the drug-metabolizing enzyme pathway, by treating cells or tissues that express the drug-metabolizing enzyme. Experimental data as provided in Figure 1 indicates expression in humans in the kidney (including kidney hypernephromas), liver (including fetal liver, HepG2 cell lines, and hepatocellular carcinomas), and pigmental retinal epithelium. These methods of treatment include the steps of administering a modulator of drug-metabolizing enzyme activity in a pharmaceutical composition to a subject in need of such treatment, the modulator being identified as described herein.

In yet another aspect of the invention, the drug-metabolizing enzyme proteins can be used as "bait proteins" in a two-hybrid assay or three-hybrid assay (see, e.g., U.S. Patent No. 5,283,317; Zervos *et al.* (1993) *Cell* 72:223-232; Madura *et al.* (1993) *J. Biol. Chem.* 268:12046-12054; Bartel *et al.* (1993) *Biotechniques* 14:920-924; Iwabuchi *et al.* (1993) *Oncogene* 8:1693-1696; and Brent WO94/10300), to identify other proteins,

which bind to or interact with the drug-metabolizing enzyme and are involved in drug-metabolizing enzyme activity. Such drug-metabolizing enzyme-binding proteins are likely to be drug-metabolizing enzyme inhibitors.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for a drug-metabolizing enzyme protein is fused to a gene encoding the DNA binding domain of a known transcription factor (e.g., GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a drug-metabolizing enzyme-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (e.g., LacZ) which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene which encodes the protein which interacts with the drug-metabolizing enzyme protein.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (e.g., a drug-metabolizing enzyme-modulating agent, an antisense drug-metabolizing enzyme nucleic acid molecule, a drug-metabolizing enzyme-specific antibody, or a drug-metabolizing enzyme-binding partner) can be used in an animal or other model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal or other model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein.

The drug-metabolizing enzyme proteins of the present invention are also useful to provide a target for diagnosing a disease or predisposition to disease mediated by the

peptide. Accordingly, the invention provides methods for detecting the presence, or levels of, the protein (or encoding mRNA) in a cell, tissue, or organism. Experimental data as provided in Figure 1 indicates expression in humans in the kidney (including kidney hypernephromas), liver (including fetal liver, HepG2 cell lines, and hepatocellular carcinomas), and pigmental retinal epithelium. The method involves contacting a biological sample with a compound capable of interacting with the drug-metabolizing enzyme protein such that the interaction can be detected. Such an assay can be provided in a single detection format or a multi-detection format such as an antibody chip array.

One agent for detecting a protein in a sample is an antibody capable of selectively binding to protein. A biological sample includes tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject.

The peptides of the present invention also provide targets for diagnosing active protein activity, disease, or predisposition to disease, in a patient having a variant peptide, particularly activities and conditions that are known for other members of the family of proteins to which the present one belongs. Thus, the peptide can be isolated from a biological sample and assayed for the presence of a genetic mutation that results in aberrant peptide. This includes amino acid substitution, deletion, insertion, rearrangement, (as the result of aberrant splicing events), and inappropriate post-translational modification. Analytic methods include altered electrophoretic mobility, altered tryptic peptide digest, altered drug-metabolizing enzyme activity in cell-based or cell-free assay, alteration in substrate or antibody-binding pattern, altered isoelectric point, direct amino acid sequencing, and any other of the known assay techniques useful for detecting mutations in a protein. Such an assay can be provided in a single detection format or a multi-detection format such as an antibody chip array.

*In vitro* techniques for detection of peptide include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence using a detection reagent, such as an antibody or protein binding agent. Alternatively, the peptide can be detected *in vivo* in a subject by introducing into the subject a labeled anti-peptide antibody or other types of detection agent. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard

imaging techniques. Particularly useful are methods that detect the allelic variant of a peptide expressed in a subject and methods which detect fragments of a peptide in a sample.

The peptides are also useful in pharmacogenomic analysis. Pharmacogenomics deal with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See, e.g., Eichelbaum, M. (*Clin. Exp. Pharmacol. Physiol.* 23(10-11):983-985 (1996)), and Linder, M.W. (*Clin. Chem.* 43(2):254-266 (1997)). The clinical outcomes of these variations result in severe toxicity of therapeutic drugs in certain individuals or therapeutic failure of drugs in certain individuals as a result of individual variation in metabolism. Thus, the genotype of the individual can determine the way a therapeutic compound acts on the body or the way the body metabolizes the compound. Further, the activity of drug metabolizing enzymes effects both the intensity and duration of drug action. Thus, the pharmacogenomics of the individual permit the selection of effective compounds and effective dosages of such compounds for prophylactic or therapeutic treatment based on the individual's genotype. The discovery of genetic polymorphisms in some drug metabolizing enzymes has explained why some patients do not obtain the expected drug effects, show an exaggerated drug effect, or experience serious toxicity from standard drug dosages. Polymorphisms can be expressed in the phenotype of the extensive metabolizer and the phenotype of the poor metabolizer. Accordingly, genetic polymorphism may lead to allelic protein variants of the drug-metabolizing enzyme protein in which one or more of the drug-metabolizing enzyme functions in one population is different from those in another population. The peptides thus allow a target to ascertain a genetic predisposition that can affect treatment modality. Thus, in a ligand-based treatment, polymorphism may give rise to amino terminal extracellular domains and/or other substrate-binding regions that are more or less active in substrate binding, and drug-metabolizing enzyme activation. Accordingly, substrate dosage would necessarily be modified to maximize the therapeutic effect within a given population containing a polymorphism. As an alternative to genotyping, specific polymorphic peptides could be identified.

The peptides are also useful for treating a disorder characterized by an absence of, inappropriate, or unwanted expression of the protein. Experimental data as provided in Figure 1 indicates expression in humans in the kidney (including kidney hypernephromas),

liver (including fetal liver, HepG2 cell lines, and hepatocellular carcinomas), and pigmental retinal epithelium. Accordingly, methods for treatment include the use of the drug-metabolizing enzyme protein or fragments.

### Antibodies

The invention also provides antibodies that selectively bind to one of the peptides of the present invention, a protein comprising such a peptide, as well as variants and fragments thereof. As used herein, an antibody selectively binds a target peptide when it binds the target peptide and does not significantly bind to unrelated proteins. An antibody is still considered to selectively bind a peptide even if it also binds to other proteins that are not substantially homologous with the target peptide so long as such proteins share homology with a fragment or domain of the peptide target of the antibody. In this case, it would be understood that antibody binding to the peptide is still selective despite some degree of cross-reactivity.

As used herein, an antibody is defined in terms consistent with that recognized within the art: they are multi-subunit proteins produced by a mammalian organism in response to an antigen challenge. The antibodies of the present invention include polyclonal antibodies and monoclonal antibodies, as well as fragments of such antibodies, including, but not limited to, Fab or F(ab')<sub>2</sub>, and Fv fragments.

Many methods are known for generating and/or identifying antibodies to a given target peptide. Several such methods are described by Harlow, *Antibodies*, Cold Spring Harbor Press, (1989).

In general, to generate antibodies, an isolated peptide is used as an immunogen and is administered to a mammalian organism, such as a rat, rabbit or mouse. The full-length protein, an antigenic peptide fragment or a fusion protein can be used. Particularly important fragments are those covering functional domains, such as the domains identified in Figure 2, and domain of sequence homology or divergence amongst the family, such as those that can readily be identified using protein alignment methods and as presented in the Figures.

Antibodies are preferably prepared from regions or discrete fragments of the drug-metabolizing enzyme proteins. Antibodies can be prepared from any region of the

peptide as described herein. However, preferred regions will include those involved in function/activity and/or drug-metabolizing enzyme/binding partner interaction. Figure 2 can be used to identify particularly important regions while sequence alignment can be used to identify conserved and unique sequence fragments.

An antigenic fragment will typically comprise at least 8 contiguous amino acid residues. The antigenic peptide can comprise, however, at least 10, 12, 14, 16 or more amino acid residues. Such fragments can be selected on a physical property, such as fragments correspond to regions that are located on the surface of the protein, e.g., hydrophilic regions or can be selected based on sequence uniqueness (see Figure 2).

Detection on an antibody of the present invention can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase,  $\beta$ -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^3\text{H}$ .

### Antibody Uses

The antibodies can be used to isolate one of the proteins of the present invention by standard techniques, such as affinity chromatography or immunoprecipitation. The antibodies can facilitate the purification of the natural protein from cells and recombinantly produced protein expressed in host cells. In addition, such antibodies are useful to detect the presence of one of the proteins of the present invention in cells or tissues to determine the pattern of expression of the protein among various tissues in an organism and over the course of normal development. Experimental data as provided in Figure 1 indicates that the drug-metabolizing proteins of the present invention are expressed in humans in the kidney